

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/566,679
Source: 1FwP
Date Processed by STIC: 2/10/06

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IFWP

RAW SEQUENCE LISTING

DATE: 02/10/2006

PATENT APPLICATION: US/10/566,679

TIME: 08:41:44

Input Set : A:\seq list.txt

Output Set: N:\CRF4\02102006\J566679.raw

3 <110> APPLICANT: CNRS

5 <120> TITLE OF INVENTION: NOVEL ANTI-ANGIOGENIC AGENT AND ITS USE, IN
PARTICULAR

6 WITHIN THE FRAMEWORK OF THE TREATMENT OF CANCER

8 <130> FILE REFERENCE: 1487-28

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/566,679

11 <141> CURRENT FILING DATE: 2006-02-01

13 <150> PRIOR APPLICATION NUMBER: PCT/FR04/02050

14 <151> PRIOR FILING DATE: 2004-07-30

16 <150> PRIOR APPLICATION NUMBER: FR 03/09506

17 <151> PRIOR FILING DATE: 2003-08-01

19 <160> NUMBER OF SEQ ID NOS: 12

21 <170> SOFTWARE: PatentIn version 3.1

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 2389

25 <212> TYPE: DNA

26 <213> ORGANISM: homo sapiens

28 <220> FEATURE:

29 <221> NAME/KEY: CDS

30 <222> LOCATION: (73)..(1143)

32 <400> SEQUENCE: 1

33 gggaaggcga gcagtgccaa tctacagcga agaaagtctc gtttggtaaa agcgagaggg 60

35 gaaagcctga gc atg cag agt gtg cag agc acg agc ttt tgt ctc cga aag 111

36 Met Gln Ser Val Gln Ser Thr Ser Phe Cys Leu Arg Lys

37 1 5 10

39 cag tgc ctt tgc ctg acc ttc ctg ctt ctc cat ctc ctg gga cag gtc 159

40 Gln Cys Leu Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val

41 15 20 25

43 gct gcg act cag cgc tgc cct ccc cag tgc ccg ggc cgg tgc cct gcg 207

44 Ala Ala Thr Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala

45 30 35 40 45

47 acg ccg ccg acc tgc gcc ccc ggg gtg cgc gcg gtg ctg gac ggc tgc 255

48 Thr Pro Pro Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys

49 50 55 60

51 tca tgc tgt ctg gtg tgt gcc cgc cag cgt ggc gag agc tgc tca gat 303

52 Ser Cys Cys Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp

53 65 70 75

55 ctg gag cca tgc gac gag agc agt ggc ctc tac tgt gat cgc agc gcg 351

56 Leu Glu Pro Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala

57 80 85 90

59 gac ccc agc aac cag act ggc atc tgc acg gcg gta gag gga gat aac 399

60 Asp Pro Ser Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn

61 95 100 105

63 tgt gtg ttc gat ggg gtc atc tac cgc agt gga gag aaa ttt cag cca 447

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64 Cys Val Phe Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro
65 110 115 120 125
67 agc tgc aaa ttc cag tgc acc tgc aga gat ggg cag att ggc tgt gtg 495
68 Ser Cys Lys Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val
69 130 135 140
71 ccc cgc tgt cag ctg gat gtg cta ctg cct gag cct aac tgc cca gct 543
72 Pro Arg Cys Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala
73 145 150 155
75 cca aga aaa gtt gag gtg cct gga gag tgc tgt gaa aag tgg atc tgt 591
76 Pro Arg Lys Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys
77 160 165 170
79 ggc cca gat gag gag gat tca ctg gga ggc ctt acc ctt gca gct tac 639
80 Gly Pro Asp Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr
81 175 180 185
83 agg cca gaa gcc acc cta gga gta gaa gtc tct gac tca agt gtc aac 687
84 Arg Pro Glu Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn
85 190 195 200 205
87 tgc att gaa cag acc aca gag tgg aca gca tgc tcc aag agc tgt ggt 735
88 Cys Ile Glu Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly
89 210 215 220
91 atg ggg ttc tcc acc cgg gtc acc aat agg aac cgt caa tgt gag atg 783
92 Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met
93 225 230 235
95 ctg aaa cag act cgg ctg tgc atg gtg cgg ccc tgt gaa caa gag cca 831
96 Leu Lys Gln Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln Glu Pro
97 240 245 250
99 gag cag cca aca gat aag aaa gga aaa aag tgt ctc cgc acc aag aag 879
100 Glu Gln Pro Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys
101 255 260 265
103 tca ctc aaa gcc atc cac ctg cag ttc aag aac tgc acc agc ctg cac 927
104 Ser Leu Lys Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His
105 270 275 280 285
107 acc tac aag ccc agg ttc tgt ggg gtc tgc agt gat ggc cgc tgc tgc 975
108 Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys
109 290 295 300
111 act ccc cac aat acc aaa acc atc cag gca gag ttt cag tgc tcc cca 1023
112 Thr Pro His Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro
113 305 310 315
115 ggg caa ata gtc aag aag cca gtg atg gtc att ggg acc tgc acc tgt 1071
116 Gly Gln Ile Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys
117 320 325 330
119 cac acc aac tgt cct aag aac aat gag gcc ttc ctc cag gag ctg gag 1119
120 His Thr Asn Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu
121 335 340 345
123 ctg aag act acc aga ggg aaa atg taacctatca ctcaagaagc acacctacag 1173
124 Leu Lys Thr Thr Arg Gly Lys Met
125 350 355
128 agcacctgta gctgctgcgc caccacccat caaaggaata taagaaaagt aatgaagaat 1233
129 cagcatttca tccttgaatc ctatgtatatt tcctaagtgt atcatatgag gacctttcat 1293

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130 atctgtcttt tattaacaa aaaatgtaat taactgtaaa cttggaatca aggtaagctc 1353
131 aggatatggc ttaggaatga cttactttcc tgtggtttta ttacaaatgc aaattttctat 1413
132 aaatttaaga aaacaagtat ataatttact ttgtagactg tttcacattg cactcatcat 1473
133 attttgttgt gcactagtgc aattccaaga aaatatcact gtaatgagtc agtgaagtct 1533
134 agaatacatc ttaacatttc attgtacaag tattacaacc atatattgag gttcattggg 1593
135 aagattctct attggctccc tttttgggta aaccagctct gaacttccaa gctccaaatc 1653
136 caaggaaaca tgcagctctt caacatgaca tccagagatg actattactt ttctgtttag 1713
137 ttttacacta ggaaacgtgt tgtatctaca gtaatgaaat gtttactaag tggactgggtg 1773
138 tcataaactt tctccattta agacacattg actcctttcc aatagaaaga aactaaacag 1833
139 aaaactccca atacaaagat gactgggtccc tcatagccct cagacattta tatattggaa 1893
140 gctgctgagg cccccaagtt ttttaattaa gcagaaacag catattagca gggattctct 1953
141 catctaactg atgagtaaac tgaggcccaa agcacttgct tacatcctct gatagctggt 2013
142 tcaaatgtgc attttgtgga attttgagaa aaatagagca aaatcaacat gactggtggt 2073
143 gagagaccac acattttatg agagtttgga attattgtag acatgcccaa aacttatcct 2133
144 tggggccataa ttatgaaaac tcatgatcaa gatatatgtg tatacataca tgtatctggt 2193
145 ttgtcaggct acaaggtagg ctgcaaaatt aaatctagac attccttttaa tgccaccaca 2253
146 cgtgttccgc ttctctcttt taaagtattt ataaaaatat aaattgtaca ttttgtaaaa 2313
147 tattatgttt gatttctcta cttgtcatat cactaaataa acacgatttt attgctgaaa 2373
148 aaaaaaaaaa aaaaaa 2389

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151 <210> SEQ ID NO: 2

152 <211> LENGTH: 357

153 <212> TYPE: PRT

154 <213> ORGANISM: homo sapiens

156 <400> SEQUENCE: 2

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157 Met Gln Ser Val Gln Ser Thr Ser Phe Cys Leu Arg Lys Gln Cys Leu
158 1 5 10 15
160 Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val Ala Ala Thr
161 20 25 30
163 Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro
164 35 40 45
166 Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys
167 50 55 60
169 Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro
170 65 70 75 80
172 Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser
173 85 90 95
175 Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn Cys Val Phe
176 100 105 110
178 Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro Ser Cys Lys
179 115 120 125
181 Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val Pro Arg Cys
182 130 135 140
184 Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala Pro Arg Lys
185 145 150 155 160
187 Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys Gly Pro Asp
188 165 170 175
190 Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr Arg Pro Glu
191 180 185 190
193 Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn Cys Ile Glu

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194          195          200          205
196 Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly Met Gly Phe
197          210          215          220
199 Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met Leu Lys Gln
200 225          230          235          240
202 Thr Arg Leu Cys Met Val Arg Pro Cys Glu Glu Pro Glu Gln Pro
203          245          250          255
205 Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys Ser Leu Lys
206          260          265          270
208 Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His Thr Tyr Lys
209          275          280          285
211 Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys Thr Pro His
212          290          295          300
214 Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro Gly Gln Ile
215 305          310          315          320
217 Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys His Thr Asn
218          325          330          335
220 Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu Leu Lys Thr
221          340          345          350
223 Thr Arg Gly Lys Met
224          355

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227 <210> SEQ ID NO: 3

228 <211> LENGTH: 216

229 <212> TYPE: DNA

230 <213> ORGANISM: Artificial sequence

232 <220> FEATURE:

233 <221> NAME/KEY: CDS

234 <222> LOCATION: (1)..(216)

236 <220> FEATURE:

237 <223> OTHER INFORMATION: Description of Artificial Sequence: fragment of

NOV protein

239 <400> SEQUENCE: 3

240 cag cgc tgc cct ccc cag tgc ccg ggc cgg tgc cct gcg acg ccg ccg 48

241 Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro

242 1 5 10 15

244 acc tgc gcc ccc ggg gtg cgc gcg gtg ctg gac ggc tgc tca tgc tgt 96

245 Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys

246 20 25 30

249 ctg gtg tgt gcc cgc cag cgt ggc gag agc tgc tca gat ctg gag cca 144

250 Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro

251 35 40 45

253 tgc gac gag agc agt ggc ctc tac tgt gat cgc agc gcg gac ccc agc 192

254 Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser

255 50 55 60

257 aac cag act ggc atc tgc acg gcg 216

258 Asn Gln Thr Gly Ile Cys Thr Ala

259 65 70

262 <210> SEQ ID NO: 4

263 <211> LENGTH: 72

264 <212> TYPE: PRT

RAW SEQUENCE LISTING

DATE: 02/10/2006

PATENT APPLICATION: US/10/566,679

TIME: 08:41:44

Input Set : A:\seq list.txt

Output Set: N:\CRF4\02102006\J566679.raw

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265 <213> ORGANISM: artificial sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: fragment of NOV protein
270 <400> SEQUENCE: 4
271 Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro
272 1 5 10 15
274 Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys
275 20 25 30
277 Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro
278 35 40 45
280 Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser
281 50 55 60
283 Asn Gln Thr Gly Ile Cys Thr Ala
284 65 70
287 <210> SEQ ID NO: 5
288 <211> LENGTH: 201
289 <212> TYPE: DNA
290 <213> ORGANISM: artificial sequence
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
294 <222> LOCATION: (1)..(201)
297 <220> FEATURE:
298 <223> OTHER INFORMATION: fragment of NOV protein
300 <400> SEQUENCE: 5
301 gat aac tgt gtg ttc gat ggg gtc atc tac cgc agt gga gag aaa ttt 48
302 Asp Asn Cys Val Phe Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe
303 1 5 10 15
305 cag cca agc tgc aaa ttc cag tgc acc tgc aga gat ggg cag att ggc 96
306 Gln Pro Ser Cys Lys Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly
307 20 25 30
310 tgt gtg ccc cgc tgt cag ctg gat gtg cta ctg cct gag cct aac tgc 144
311 Cys Val Pro Arg Cys Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys
312 35 40 45
314 cca gct cca aga aaa gtt gag gtg cct gga gag tgc tgt gaa aag tgg 192
315 Pro Ala Pro Arg Lys Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp
316 50 55 60
318 atc tgt ggc 201
319 Ile Cys Gly
320 65
323 <210> SEQ ID NO: 6
324 <211> LENGTH: 67
325 <212> TYPE: PRT
326 <213> ORGANISM: artificial sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: fragment of NOV protein
331 <400> SEQUENCE: 6
332 Asp Asn Cys Val Phe Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe
333 1 5 10 15
335 Gln Pro Ser Cys Lys Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/566,679

DATE: 02/10/2006

TIME: 08:41:45

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L:10 M:270 C: Current Application Number differs, Replaced Current Application
Number